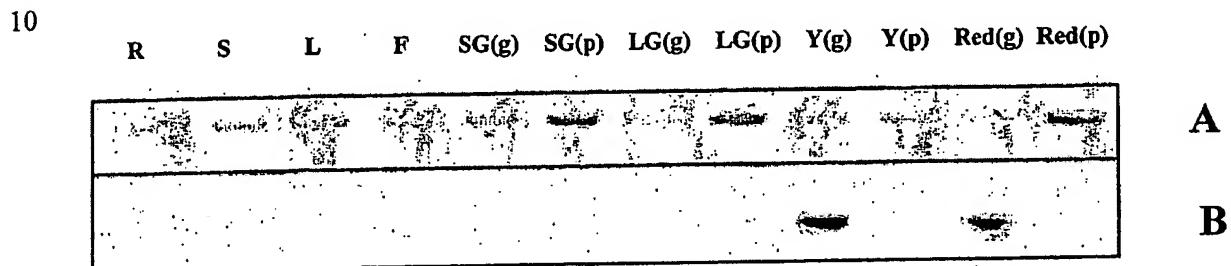
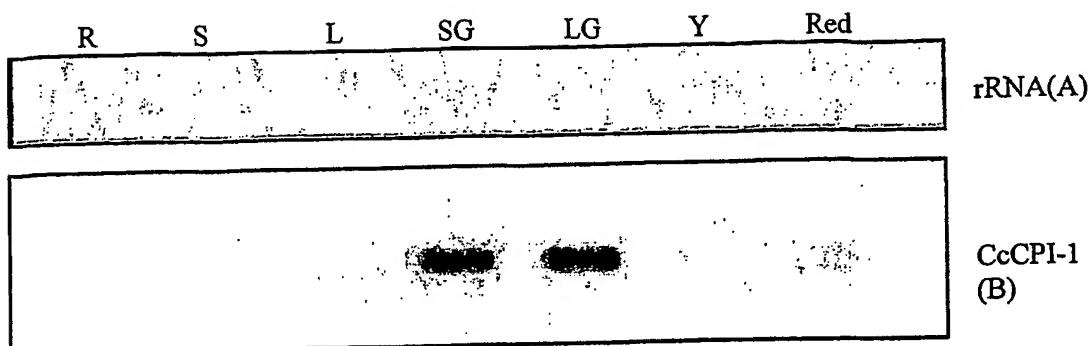


5 **Figure 1:** Northern blot analysis of the expression of the cysteine proteinase (CcCP1) gene in different tissues of *Coffea arabica*.



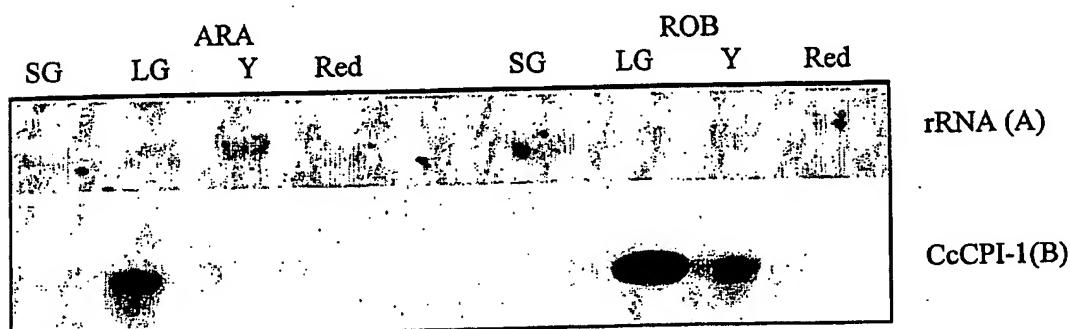
10  
15 **Figure 2:** Northern blot analysis of the expression of the Cysteine proteinase CcCP-1 gene in different tissues of *Coffea arabica*.

**Figure 2A:** Alignment of the full sequence of the protein encoded by CccP-1 cDNA with other full-length cysteine proteinases available in the NCBI database.

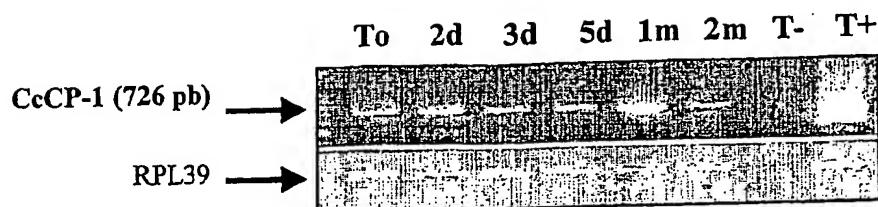


5 **Figure 3:** Northern blot analysis of the expression of the cysteine proteinase inhibitor (CcCPI-1) gene in different tissues of *Coffea arabica*.

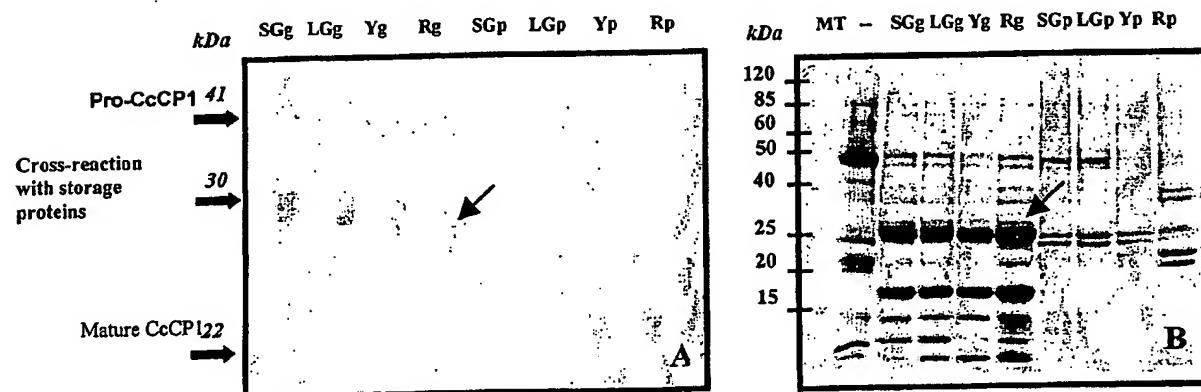
10



**Figure 4:** Northern blot analysis of the expression of the cysteine proteinase inhibitor gene (CcCPI-1) at different cherry development stages for *Coffea arabica* (ARA) and *Coffea canephora* (ROB).



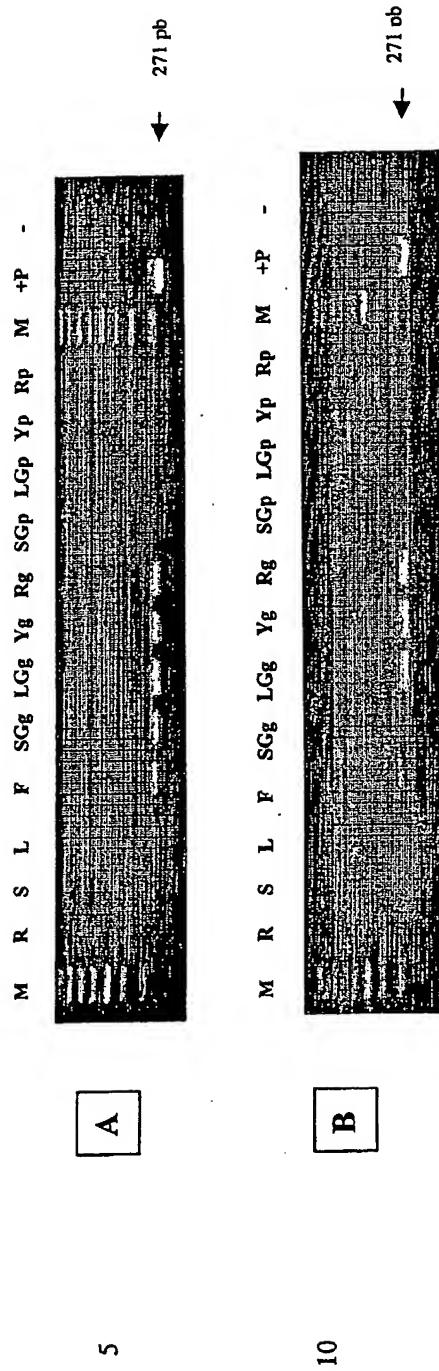
**Figure 5.** RT-PCR analysis of the expression of *CcCP-1* during *Coffea arabica* grain germination.



**Figure 6:** Western-blot analysis of the expression of CcCP1 protein (A).

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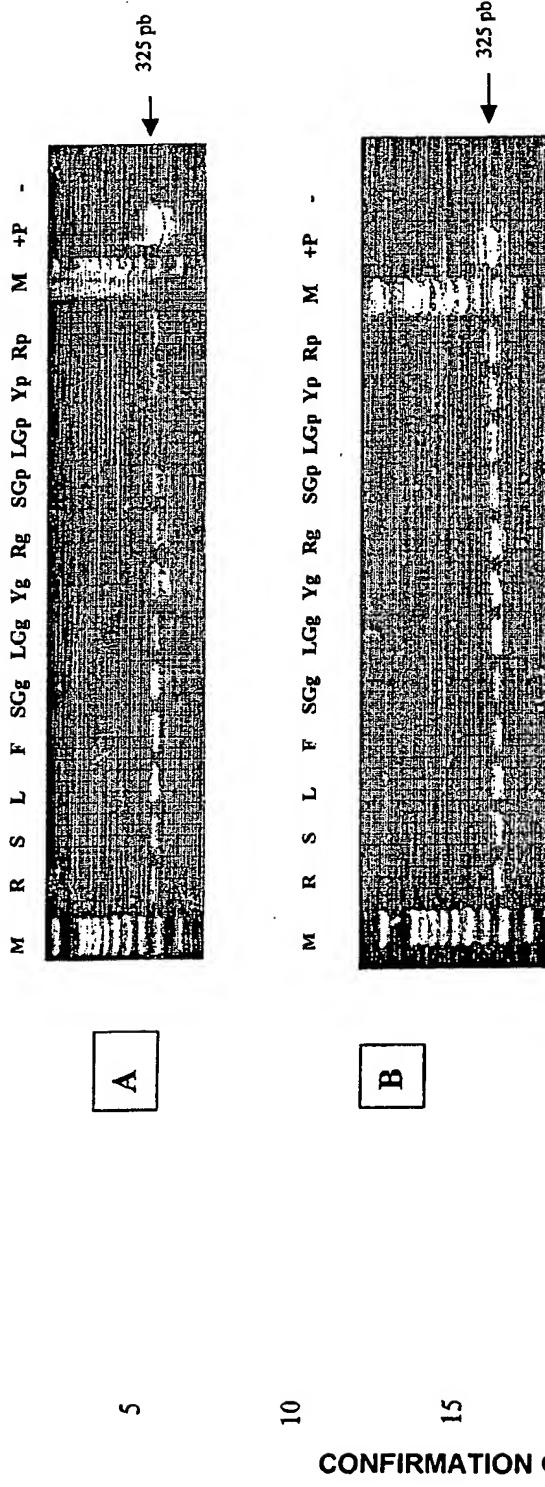
**Figure 6A:** Optimal alignment of the complete protein encoded by CcCPI-1 cDNA with other homologous full-length cysteine proteinases available in the NCBI.



15 - Figure 7: RT-PCR analysis of the expression of CcCPI-1 gene in different tissues of *Coffea arabica* CCCA2 (A) and *Coffea robusta* FRT-32 (B).

<pre> 1 M A K V G G I S E S K G N - E N S I L E : ! E S I L A K I F A V D D Y N K K Q N A L L E 1 M A T I G G I K Q V E G S - A N S I L E V E S L A K F A V E D H N K K Q N A M L E 1 M A T . V G G I K D S G S S A N S I L E I I D E L A K F A V D H Y I N S K E N A L L E 1 M A T L G G I K E V E S - A N S V E I D N L A R F A V D D Y N K K Q N A L L F </pre>	<pre> CcCPI-2 R. obusifolius D. caryophylus M. esculenta </pre>
<pre> 40 F Q K V I N S K E I Q V V A G T V Y Y L T I E V K K L Y E A K V W V K P 40 F S K V V I N T K E Q V V A G T M Y Y I T L E I A T D G G K K V Y E A K V W V K P 41 F Q R V V N T K E Q V V A G T I Y Y I T L E A T D G G V K K L Y E A K V W V K P 40 F K R V V S T K Q Q V V A G T M Y Y I T L E V A D G G Q T K V Y E A K V W E K P </pre>	<pre> CcCPI-2 R. obusifolius D. caryophylus M. esculenta </pre>
<pre> 80 W L : N I F I K E V Q E F K P A A G D T S A 80 W M N I F I K Q V I Q E F I K L L G D Q G S T S 81 W V N . F . K . E V Q D F K Y V G D A S A 80 W L N F K E V Q E F K P I G V A P S D S T A </pre>	<pre> CcCPI-2 R. obusifolius D. caryophylus M. esculenta </pre>

Figure 8: Optimal alignment of the complete protein encoded by CcCPI-2 cDNA with other homologous full-length cysteine proteinases available in the NCBI.



20      Figure 9: RT-PCR analysis of the expression of CcCPI-2 gene in different tissues of *Coffea arabica CCCA2* (A) and *Coffea robusta* FRT-32 (B).

**Figure 10:** Optimal alignment of the complete protein encoded by CcCPI-3 cDNA with other homologous full-length cysteine proteinases available in the NCBI.

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<pre> 1 M A T V A A K S A T A A I G A G Q K N M V G G L S S T V P P R S S T Y N P K D I P H V I Q 1 M N Q R F C C L I V L F A G D R K Q A L V G I G I W K P I E D P K E V M E Citrus x paradisi 1 M T S K V V F L L L P L Y A S A A R V G G W S S P I S N V T D P Q V V E A. thaliana </pre>	<pre> 46 I A Q F :A :V A N Y N A K A Q T T V V W L N V .E Y G F W W I D D T Y Y M L A I K T Q D L T CcCPI-4 46 I G Q F :A :V T E Y :N ;K Q S A L K F :E S V E K Q .E .T .Q .V .S .G .T .N .Y .R .L .I .L .V .V .K .D .G .P Citrus x paradisi 45 I G E F A V S F A V S F E Y N K R S P S Q L K F E T V V S G .E .T .Q .V .S .G .T .N .Y .R .L .K .V .A .A .N .D .G .D A. thaliana </pre>	<pre> 91 - G T H C D V A L Y R E I S E S N Q T Y S L K W Y N H N N K CcCPI-4 91 - S T E K F E A V V .W .E K P .W E H - F K S L T S F K P M V K Citrus x paradisi 90 G V S K N Y L A I V W D K P W M K - F R N L T S F E P A N N G R F L A. thaliana </pre>
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Figure 11: Optimal alignment of the complete protein encoded by CcCPI-4 cDNA with other homologous full-length cysteine proteinases available in the NCBI.

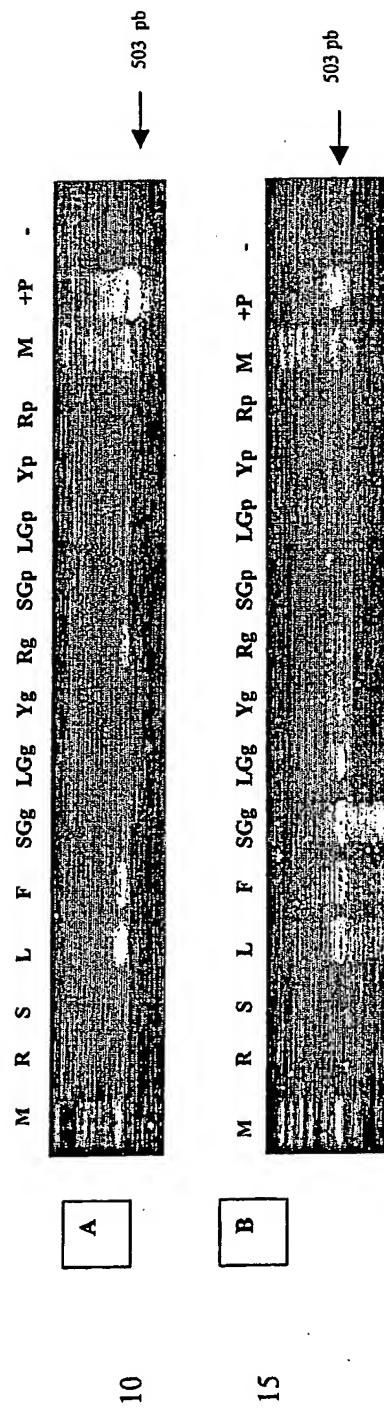


Figure 12: RT-PCR analysis of the expression of CcCPI-4 gene in different tissues of *Coffea arabica* CCCA2 (Panel A) and of *Coffea robusta* FRT-32 (Panel B)



Figure 13: Northern blot analysis of the expression of the aspartic proteinase 2 (CcAP2) gene in different tissues of *Coffea arabica*.

1 gcttacatcttaatccgtatTTTatAGATTcgcCTTCgtgaAGTtcAATCTCGCAGTCGCTcaCTAACATTTGGT  
 81 agacataCTCGATT ATG AAA ATG GGG AAG GCT TTC CTT TTT GCC GTT GTA TTG GCT GTG ATC  
 1 M K M G K A F L P A V V L A V I  
 144 TTA GTG GCG GCT ATG AGC ATG GAG ATC ACA GAA AGA GAT TTG GCT TCT GAG GAA AGC TTG  
 17 L V A A M S M E I T E R D L A S E E S L  
 204 TGG GAC TTG TAC GAA AGA TGG AGG AGC CAT CAT ACT GTT TCT CGA GAC CTT TCT GAG AAA  
 37 W D L Y E R W R S H H T V S R D L S B K  
 264 CGA AAG CGC TTT AAT GTT TTC AAG GCA AAT GTC CAT CAC ATT CAC AAG GTG AAC CAG AAG  
 57 R K R F N V F K A N V H H I H K V N Q K  
 324 GAC AAG CCT TAC AAG CTG AAA CTC AAC AGT TTC GCT GAT ATG ACC AAC CAC GAG TTC AGG  
 77 D K P Y K L K L N S F A D M T N H E F R  
 384 GAA TTC TAC AGT TCT AAG GTG AAA CAT TAC CGG ATG CTC CAC GGC AGT CGT GCT AAT ACT  
 97 E F Y S S K V K H Y R M L H G S R A N T  
 444 GGA TTT ATG CAT GGG AAG ACT GAA AGT TTG CCA GCC TCC GTT GAT TGG AGA AAG CAA GGA  
 117 G F M H G K T E S L P A S V D W R K Q G  
 504 GCC GTG ACT GGC GTC AAG AAT CAA GGC AAA TGT GGT AGC TGT TGG GCA TTT TCA ACT GTG  
 137 A V T G V K N Q G K C G S C W A F S T V  
 564 GTT GGA GTC GAG GGA ATC AAC AAA ATC AAA ACA GGC CAA TTA GTT TCT CTG TCC GAG CAA  
 157 V G V E G I N K I K T G Q L V S L S E Q  
 624 GAA CTT GTT GAC TGT GAA ACG GAC AAT GAA GGA TGC AAC GGA GGA CTC ATG GAA AAT GCA  
 177 E L V D C E T D N E G C N G G L M E N A  
 684 TAC GAG TTT ATT AAG AAA AGT GGG GGA ATA ACA ACT GAG AGG CTA TAT CCC TAC AAG GCA  
 197 Y E F I K K S G G I T T E R L Y P Y K A  
 744 AGA GAT GGC AGC TGT GAT TCG TCA AAG ATG AAT GCC CCT GCT GTG ACT ATT GAT GGG CAT  
 217 R D G S C D S S K M N A P A V T I D G H  
 804 GAA ATG GTA CCC GCA AAC GAT GAG AAT GCC TTG ATG AAA GCT GTT GCT AAC CAG CCT GTA  
 237 E M V P A N D E N A L M K A V A N Q P V  
 864 TCA GTA GCT ATA GAT GCG TCT GGC TCT GAC ATG CAA TTT TAT TCA GAG GGT GTA TAC GCT  
 257 S V A I D A S G S D M Q F Y S E G V Y A  
 924 GGA GAC TCG TGT GGC AAT GAG CTT GAT CAT GGC GTG GCG GTC GTC GGC TAC GGG ACT GCT  
 277 G D S C G N E L D H G V A V V G Y G T A  
 984 CTT GAC GGT ACT AAA TAC TGG ATA GTG AAG AAC TCA TGG GGA ACA GGA TGG GGA GAA CAG  
 297 L D G T K Y W I V K N S W G T G W G E Q  
 1044 GGC TAT ATC AGG ATG CAA CGT GGT GTT GAT GCT CCT GAA GGC GGA GTT TGT GGG ATA GCA  
 317 G Y I R M Q R G V D A A E G G V C G I A  
 1104 ATG GAG GCC TCC TAT CCA CTT AAA TTG TCC TCC CAC AAT CCA AAA CCA TCC CCA CCT AAG  
 337 M B A S Y P L K L S S H N P K P S P P K  
 1164 GAC GAC CTC TAG attgatccTCTtatatacatatatataattttcagttagattcattgaatttttagttac  
 357 D D L \*  
 1240 agactacgcgttcTGAAGACTTAGATCATCTCTAGGCATAGATTATGTAATCCTGCTCTGTGATGGTTGAATAAAC  
 1320 aataagtagtactataaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

**Figure 14:** cDNA sequence and its deduced amino acid sequence of CcCP-4. Lowercase: 5' and 3' non-translated regions; Uppercase: Open reading frame; Bold character: amino acid sequence; \*: stop codon

**Figure 15:** Alignment of the full sequence of the protein encoded by CcCP-4 cDNA with other full-length cysteine proteinases available in the NCBI database.

Decoration 'Decoration #1': Shade (with solid black) residues that match KDDL -CCCP4 exactly.0

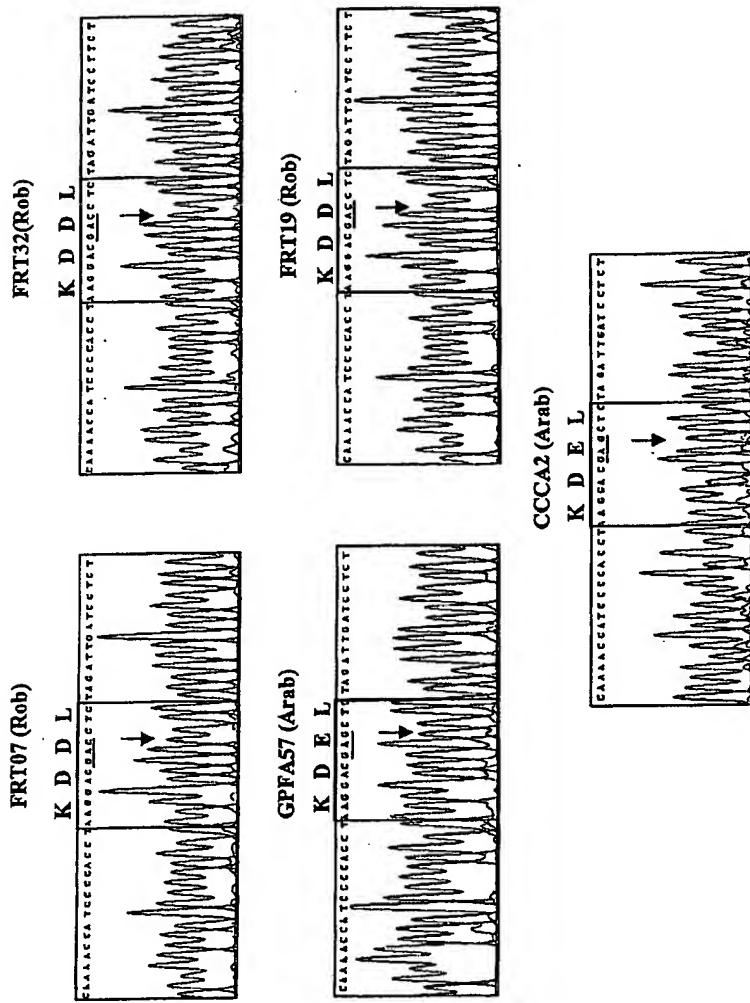
**Figure 16.** The full length cDNA sequence CcCP-4 KDDL and the partial cDNA sequence CcCP-4 (KBEL).

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5           **K**KNGKAFLFENVVAVILVAAMSMEITERD~~L~~A~~E~~ESLWDLYEP~~R~~SHHTVSRDLSEKRKFNVKANVRH~~I~~HKVNVQKD~~P~~Y  
**1**           **K**LKLNSFA~~D~~ITNHEFREFYSSKVFKHYRM~~L~~HGSRANTGFMH~~G~~KTESL~~P~~ASV~~D~~W~~R~~KQGAVTGVKNQGKC~~S~~CWA,~~F~~~~S~~T~~V~~~~N~~~~G~~  
**1**           **G**INKI~~K~~TGQI~~V~~SL~~S~~EQELV~~D~~CETDNEGCNGGLMENAWAEFIKKSGGITTTER~~R~~YP~~K~~ARD~~S~~CD~~S~~SS~~K~~NA~~P~~AV~~T~~ID~~G~~HENVP  
**161**           **G**INKI~~K~~TGQI~~V~~SL~~S~~EQELV~~D~~CETDNEGCNGGLMENAWAEFIKKSGGITTTER~~R~~YP~~K~~ARD~~S~~CD~~S~~SS~~K~~NA~~P~~AV~~T~~ID~~G~~HENVP  
**17**           **A**NDENALM~~M~~KIAVANQ~~P~~VSAYAIDASGS~~D~~SD~~W~~Q~~Y~~SEGVYAGDS~~C~~GN~~E~~UHGVAVN~~V~~GT~~A~~UD~~G~~T~~K~~Y~~W~~IVKNS~~W~~~~T~~G~~W~~GEQ~~Q~~Y~~I~~R  
**241**           **A**NDENALM~~M~~KIAVANQ~~P~~VSAYAIDASGS~~D~~SD~~W~~Q~~Y~~SEGVYAGDS~~C~~GN~~E~~UHGVAVN~~V~~GT~~A~~UD~~G~~T~~K~~Y~~W~~IVKNS~~W~~~~T~~G~~W~~GEQ~~Q~~Y~~I~~R  
**97**           **M**QRGVDA~~A~~EGGVCGIANEA~~S~~YPLKLS~~H~~NPKPSPPKDDI  
**321**           **M**QRGVDA~~A~~EGGVCGIANEA~~S~~YPLKLS~~H~~NPKPSPPKDDI  
**177**           **M**QRGVDA~~A~~EGGVCGIANEA~~S~~YPLKLS~~H~~NPKPSPPKDDI

Decoration '#1': shade (with solid black) residues that match CcCP-4 KDDI exactly.

Figure 17. The complete open reading frame of CcCP-4 (KDDL) and the partial open reading frame of CcCP-4 (KDEL).



5 Figure 18. DNA sequence chromatograms for PCR amplified genomic DNA encoding the KDEL/KDDDL region of the CcCP-4 gene.

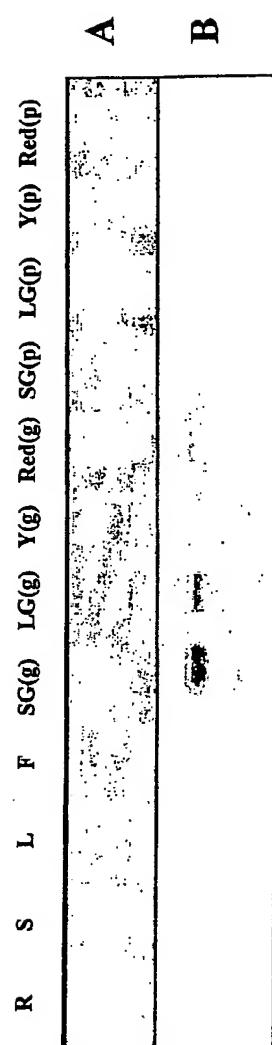
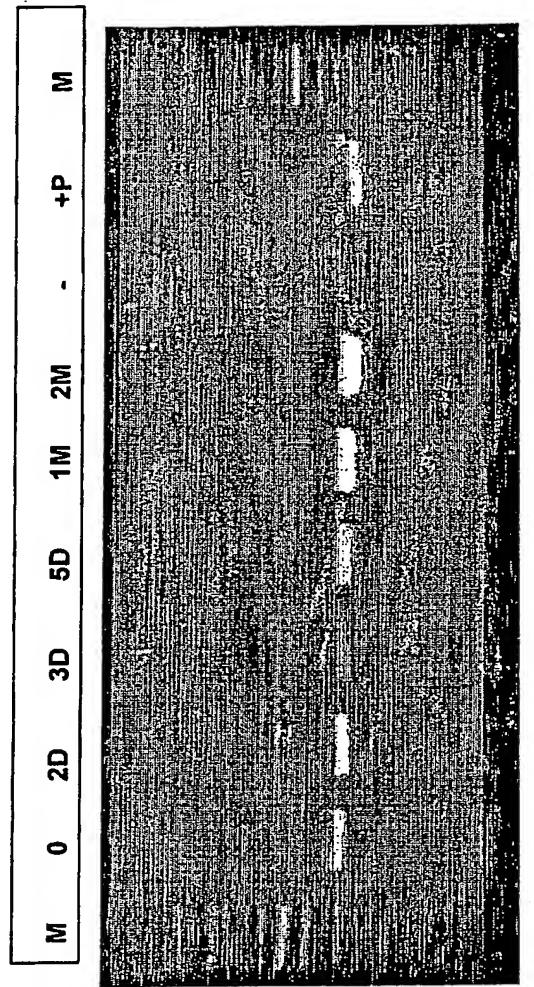


Figure 19. Northern blot analysis of the expression of the Cysteine proteinase CcCP-4 gene in different tissues of *Coffea arabica*.



**Figure 20.** RT-PCR analysis of the expression of CcCP-4 in the whole grain during germination.

161 M L A L D I M P L G N G S P T D A L V F T K L S I G C A P H  
162 M D P S R I R I V A V V P V L V I Q V Y S O N V P N Y T K P A C K E R Q L S B L K S W D S P R H A R L A N I H L P L G G D S R A D S I G Y T K K I G C A P H (BARD 360)  
163 T U P Q D V Y V V Q D T G G D L W V N C A G V V R C K E S B L G D I T I Y O M M A S S I Q R L V T I D Q F C I S A M P A S D L S K V O H P C A Y S T Y C A P H  
164 T S P K E R V Q D V D S I L W N C A P F K C V T D Q T P E A V D V D I T S S I S S I K N O C D U C S - T M Q S E T I C A R K C U S Y H V V Y A P H (BARD 360)  
165 10 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
166 11 J D G S S T S Q D F I K D N T L E U V T G N R T A P L A Q E V V F G C K N H A R I N Q L G Q T D S A V D G I N U F C O S I N S I S I L S U L K A Q G S T I N R I F S H I P A P H (BARD 360)  
167 12 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
168 13 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
169 14 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
170 15 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
171 16 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
172 17 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
173 18 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
174 19 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
175 20 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
176 21 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
177 22 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
178 23 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
179 24 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
180 25 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
181 26 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
182 27 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
183 28 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
184 29 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
185 30 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
186 31 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
187 32 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
188 33 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
189 34 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H  
190 35 J D G S S T N G C Y L K D V H D I K D N T S Q D F C I S S I S S I L G Q A N S S L I S Q U L S A Q S V X K L F A H C A P H

**Figure 21:** Optimal alignment of the complete protein encoded by CcAP-1 cDNA with other homologous full-length aspartic proteinase sequences available in the NCBI.

1	MERRYLLWAFAVLGRIVCSLFPLPSEG-LKRISLKKPLDIOSSIRRAAKLAHLESTHGAAGRKE 1	CCAP2
1	MGCKHHLVTVFCLWATCSSLFESFSFG-IIRLGLKKRPLDLSIARRKAREGLRSVRPMGAEQFT 1	G.max
1	MGKRYLCAFLLWAVCTZELPAYSNDNLERVGLKRPEDDLSEIKAKRKGRRLGGKYKGKGVN- 1	I. batatas
1	KDRRHLCAFLLWAVCTZELPAYSNDNLERVGLKRPEDDLSEIKAKRKGRRLGGKYKGKGVN- 1	-KKKL
1	MGHRRNLWVIEFCFAUJISCFESTSDGE--LVRIGLKRQFSDNSIRRAVTRKAGHN-QGLKRF-QYSFN 1	N. elatia N
66	GSSN-EDILPLKNYLDDAQYXYGEIGIGTDPQXKFVNIEDTGSNNLWUFSAKCYPSSLACWLHSK 66	CCAP2
67	GKSKGEDIVPLKNYLDAQYFGRIGIGTDPQXKFVNIEDTGSNNLWUFSAKCYPSSLACWLHSK 67	G.max
65	GDSD-TYKVPPLKNYLDDAQYXYGEISIGSIPQONFTV1FEDTGSSNNLWUFSAKCYPSSLACWLHS 65	I. batatas
65	GDSD-TD.IVYLRVYLDAQYXYGEIGIGTDPQXKFVNIEDTGSNNLWUFSAKCYPSSLACWLHSK 65	I. esculentum
65	GDSD-TD.IVYLRVYLDAQYXYGEIGIGTDPQXKFVNIEDTGSNNLWUFSAKCYPSSLACWLHSK 65	N. elatia N
133	TYTATIGKSCSIRYGSISGESSQ.DNVEYGD.LVVKD.QVFILEAGREGSLLTVEIAKEDGILGLGP 133	CCAP2
135	THVNGTSCKRINYGTGTSISGEFESQ.DNWKVGSSAVVQDQVLDLVLKQDVFEETTRPSLT 135	G.max
133	TYTATIGKSCSIRYGTGTSISGEFESQ.DNWKVGSSAVVQDQVLDLVLKQDVFEETTRPSLT 133	I. batatas
133	TYTATIGKSCSIRYGTGTSISGEFESQ.DNWKVGSSAVVQDQVLDLVLKQDVFEETTRPSLT 133	I. esculentum
133	TYTATIGKSCSIRYGTGTSISGEFESQ.DNWKVGSSAVVQDQVLDLVLKQDVFEETTRPSLT 133	N. elatia N
201	DNMUPWVYNNMVDQGLYDEQEFSEFWLNRDIPNAEDEGELVIFGVDINHFKGKHHTV 201	CCAP2
203	EHAIVPVWFKMVEQOKLISEKVSFSEWLNRDIPNAEDEGELVIFGVDINHFKGKHHTV 203	G.max
200	ENVWVWYDWTQGKSCSIRYGTGTSISGEFESQ.DNWKVGSSAVVQDQVLDLVLKQDV 200	I. batatas
201	GHTTPVWVUNVQGKSCSIRYGTGTSISGEFESQ.DNWKVGSSAVVQDQVLDLVLKQDV 201	I. esculentum
200	GDPVWVUNVQGKSCSIRYGTGTSISGEFESQ.DNWKVGSSAVVQDQVLDLVLKQDV 200	N. elatia N
269	FIGNVSTGFCEGGCAARIYDSGTSLLAGFTPVVTOINHAAIGNEGVNSTEICKEV 269	CCAP2
271	FEVCGVSTGFCEGGCAARIYDSGTSLLAGFTPVVTOINHAAIGNEGVNSTEICKEV 271	G.max
268	FIGNVSTGFCEGGCAVTDGSITGPTAVVTEINAYTAIGPEGVVCAECKEV 268	I. batatas
269	FIGNVSTGFCAGGCAARIYDSGTSLLAGFTPVVTOINHAAIGNEGVNSTEICKEV 269	I. esculentum
266	FIGNVSTGFCAGGCAARIYDSGTSLLAGFTPVVTOINHAAIGNEGVNSTEICKEV 266	N. elatia N
337	VLPDRVCKQAGLCPLRGAOHENRAYLNSVDELENKEASSVGESMCCTACE 337	CCAP2
339	TKPDDIVCSQVGECSKRGQSRSAGIEWTERKQ-EELA 339	G.max
337	TRADIVCSQVGECSKRGQSRSAGIEWTERKQ-EELA 337	I. batatas
337	TRADIVCSQVGECSKRGQSRSAGIEWTERKQ-EELA 337	I. esculentum
336	VOPDKICSQLACFCN-DAQFLSIGKTVIERENRKN3VALDFLC 336	N. elatia N
405	LAYVNQLCESISPNSPGESETIYDCNSLSITLPRNVSETLGGRSFELTLKEYV 405	CCAP2
339	TKPDDIVCSQVGECSKRGQSRSAGIEWTERKQ-EELA 339	I. batatas
406	FNYVNQLCSESHPSPSGESVISCNLSKMPNTFTIGNKPEVLTPEQYLLRT 406	I. batatas
404	LEYVNQLCESHPSPDGESVISCNLSKMPNTFTIGNKPEVLTPEQYLLRT 404	I. esculentum
403	LEYVNQLCESHPSPDGESVISCNLSKMPNTFTIGNKPEVLTPEQYLLRT 403	N. elatia N
473	PFPFRGFIWVVLGDFVNGYHTYFDTYGNLRMGFA 473	CCAP2
474	PPPKGPPLWILGDVFYRAYHTVFDYGNLUVGF 474	G.max
472	PPPOGPGLWILGDVFYRAYHTVFDYGNLUVGF 472	I. batatas
472	PPPPGPGLWILGDVFYRAYHTVFDYGNLUVGF 472	I. esculentum
471	PPPSGPGLWILGDVFYRAYHTVFDYGNLUVGF 471	N. elatia N

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